



Post-Transcriptional Regulation of Homeostatic, Stressed, and Malignant Stem Cells.

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Public Summary:

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Scientific Abstract:

Cellular identity is not driven by differences in genomic content but rather by epigenomic, transcriptomic, and proteomic heterogeneity. Although regulation of the epigenome plays a key role in shaping stem cell hierarchies, differential expression of transcripts only partially explains protein abundance. The epitranscriptome, translational control, and protein degradation have emerged as fundamental regulators of proteome complexity that regulate stem cell identity and function. Here, we discuss how post-transcriptional mechanisms enable stem cell homeostasis and responsiveness to developmental cues and environmental stressors by rapidly shaping the content of their proteome and how these processes are disrupted in pre-malignant and malignant states.

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